



OICE

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/444,711A

DATE: 11/29/2002 P.6  
TIME: 16:04:03

Input Set : A:\USF-T136.ST25.txt

Output Set: N:\CRF4\11292002\I444711A.raw

3 <110> APPLICANT: Yeatman, Timothy J.  
 4 Irby, Rosalyn B.  
 6 <120> TITLE OF INVENTION: Mutated SRC Oncogene Composition and Methods  
 8 <130> FILE REFERENCE: USF-T136  
 10 <140> CURRENT APPLICATION NUMBER: US 09/444,711A  
 C--> 11 <141> CURRENT FILING DATE: 2002-11-13  
 13 <160> NUMBER OF SEQ ID NOS: 7  
 15 <170> SOFTWARE: PatentIn version 3.1  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 1611  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Homo sapiens  
 22 <220> FEATURE:  
 23 <221> NAME/KEY: misc\_feature  
 24 <222> LOCATION: (1)..(1611)  
 25 <223> OTHER INFORMATION: nucleotide sequence of normal c-Src oncogene coding region  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (1)..(1611)  
 31 <223> OTHER INFORMATION:  
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 35 atg ggt agc aac aag agc aag ccc aag gat gcc agc cag cgg cgc cgc 48  
 36 Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg  
 37 1 5 10 15  
 39 agc ctg gag ccc gcc gag aac gtg cac ggc gct ggc ggg ggc gct ttc 96  
 40 Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe  
 41 20 25 30  
 43 ccc gcc tcg cag acc ccc agc aag cca gcc tcg gcc gac ggc cac cgc 144  
 44 Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg  
 45 35 40 45  
 47 ggc ccc agc gcg gcc ttc gcc ccc gcg gcc gcc gag ccc aag ctg ttc 192  
 48 Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe  
 49 50 55 60  
 51 gga ggc ttc aac tcc tcg gac acc gtc acc tcc ccg cag agg gcg ggc 240  
 52 Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly  
 53 65 70 75 80  
 55 ccg ctg gcc ggt gga gtg acc acc ttt gtg gcc ctc tat gac tat gag 288  
 56 Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu  
 57 85 90 95  
 59 tct agg acg gag aca gac ctg tcc ttc aag aaa ggc gag cgg ctc cag 336  
 60 Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln  
 61 100 105 110  
 63 att gtc aac aac acg gag gga gac tgg tgg ctg gcc cac tcg ctc agc 384

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64	Ile	Val	Asn	Asn	Thr	Glu	Gly	Asp	Trp	Trp	Leu	Ala	His	Ser	Leu	Ser	
65			115					120					125				
67	aca	gga	cag	aca	ggc	tac	atc	ccc	agc	aac	tac	gtg	gcg	ccc	tcc	gac	432
68	Thr	Gly	Gln	Thr	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Ala	Pro	Ser	Asp	
69		130					135					140					
71	tcc	atc	cag	gct	gag	gag	tgg	tat	ttt	ggc	aag	atc	acc	aga	cgg	gag	480
72	Ser	Ile	Gln	Ala	Glu	Trp	Tyr	Phe	Gly	Lys	Ile	Thr	Arg	Arg	Glu		
73		145				150				155					160		
75	tca	gag	cgg	tta	ctg	ctc	aat	gca	gag	aac	ccg	aga	ggg	acc	ttc	ctc	528
76	Ser	Glu	Arg	Leu	Leu	Leu	Asn	Ala	Glu	Asn	Pro	Arg	Gly	Thr	Phe	Leu	
77				165						170				175			
79	gtg	cga	gaa	agt	gag	acc	acg	aaa	ggg	gcc	tac	tgc	ctc	tca	gtg	tct	576
80	Val	Arg	Glu	Ser	Glu	Thr	Thr	Lys	Gly	Ala	Tyr	Cys	Leu	Ser	Val	Ser	
81			180					185				190					
83	gac	ttc	gac	aac	gcc	aag	ggc	ctc	aac	gtg	aag	cac	tac	aag	atc	cgc	624
84	Asp	Phe	Asp	Asn	Ala	Lys	Gly	Leu	Asn	Val	Lys	His	Tyr	Lys	Ile	Arg	
85			195					200				205					
87	aag	ctg	gac	agc	ggc	ggc	ttc	tac	atc	acc	tcc	cgc	acc	cag	ttc	aac	672
88	Lys	Leu	Asp	Ser	Gly	Gly	Phe	Tyr	Ile	Thr	Ser	Arg	Thr	Gln	Phe	Asn	
89		210				215					220						
91	agc	ctg	cag	cag	ctg	gtg	gcc	tac	tac	tcc	aaa	cac	gcc	gat	ggc	ctg	720
92	Ser	Leu	Gln	Gln	Leu	Val	Ala	Tyr	Tyr	Ser	Lys	His	Ala	Asp	Gly	Leu	
93	225				230					235					240		
95	tgc	cac	cgc	ctc	acc	gtg	tgc	ccc	acg	tcc	aag	ccg	cag	act	cag		768
96	Cys	His	Arg	Leu	Thr	Val	Cys	Pro	Thr	Ser	Lys	Pro	Gln	Thr	Gln		
97			245					250				255					
99	ggc	ctg	gcc	aag	gat	gcc	tgg	gag	atc	cct	cgg	gag	tgc	ctg	cgg	ctg	816
100	Gly	Leu	Ala	Lys	Asp	Ala	Trp	Glu	Ile	Pro	Arg	Glu	Ser	Leu	Arg	Leu	
101			260					265				270					
103	gag	gtc	aag	ctg	ggc	cag	ggc	tgc	ttt	ggc	gag	gtg	tgg	atg	ggg	acc	864
104	Glu	Val	Lys	Leu	Gly	Gln	Gly	Cys	Phe	Gly	Glu	Val	Trp	Met	Gly	Thr	
105			275				280				285						
107	tgg	aac	ggt	acc	acc	agg	gtg	gcc	atc	aaa	acc	ctg	aag	cct	ggc	acg	912
108	Trp	Asn	Gly	Thr	Thr	Arg	Val	Ala	Ile	Lys	Thr	Leu	Lys	Pro	Gly	Thr	
109		290				295					300						
111	atg	tct	cca	gag	gcc	ttc	ctg	cag	gag	gcc	cag	gtc	atg	aag	aag	ctg	960
112	Met	Ser	Pro	Glu	Ala	Phe	Leu	Gln	Glu	Ala	Gln	Val	Met	Lys	Lys	Leu	
113	305				310					315					320		
115	agg	cat	gag	aag	ctg	gtg	cag	ttg	tat	gct	gtg	gtt	tca	gag	gag	ccc	1008
116	Arg	His	Glu	Lys	Leu	Val	Gln	Leu	Tyr	Ala	Val	Val	Ser	Glu	Glu	Pro	
117			325					330				335					
119	att	tac	atc	gtc	acg	gag	tac	atg	agc	aag	ggg	agt	ttg	ctg	gac	ttt	1056
120	Ile	Tyr	Ile	Val	Thr	Glu	Tyr	Met	Ser	Lys	Gly	Ser	Leu	Leu	Asp	Phe	
121			340					345				350					
123	ctc	aag	ggg	gag	aca	ggc	aag	tac	ctg	cgg	ctg	cct	cag	ctg	gtg	gac	1104
124	Leu	Lys	Gly	Glu	Thr	Gly	Lys	Tyr	Leu	Arg	Leu	Pro	Gln	Leu	Val	Asp	
125			355				360					365					
127	atg	gct	gct	cag	atc	gcc	tca	ggc	atg	gcg	tac	gtg	gag	cgg	atg	aac	1152
128	Met	Ala	Ala	Gln	Ile	Ala	Ser	Gly	Met	Ala	Tyr	Val	Glu	Arg	Met	Asn	

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129      370      375      380
131 tac gtc cac cgg gac ctt cgt gca gcc aac atc ctg gtg gga gag aac 1200
132 Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
133 385      390      395      400
135 ctg gtg tgc aaa gtg gcc gac ttt ggg ctg gct cgg ctc att gaa gac 1248
136 Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
137      405      410      415
139 aat gag tac acg gcg cgg caa ggt gcc aaa ttc ccc atc aag tgg acg 1296
140 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
141      420      425      430
143 gct cca gaa gct gcc ctc tat ggc cgc ttc acc atc aag tcg gac gtg 1344
144 Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
145      435      440      445
147 tgg tcc ttc ggg atc ctg ctg act gag ctc acc aca aag gga cgg gtg 1392
148 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val
149      450      455      460
151 ccc tac cct ggg atg gtg aac cgc gag gtg ctg gac cag gtg gag cgg 1440
152 Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg
153 465      470      475      480
155 ggc tac cgg atg ccc tgc ccg ccg gag tgt ccc gag tcc ctg cac gac 1488
156 Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
157      485      490      495
159 ctc atg tgc cag tgc tgg cgg aag gag cct gag gag cgg ccc acc ttc 1536
160 Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
161      500      505      510
163 gag tac ctg cag gcc ttc ctg gag gac tac ttc acg tcc acc gag ccc 1584
164 Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
165      515      520      525
167 cag tac cag ccc ggg gag aac ctc tag 1611
168 Gln Tyr Gln Pro Gly Glu Asn Leu
169      530      535
172 <210> SEQ ID NO: 2
173 <211> LENGTH: 536
174 <212> TYPE: PRT
175 <213> ORGANISM: Homo sapiens
177 <220> FEATURE:
178 <221> NAME/KEY: MISC_FEATURE
179 <222> LOCATION: (1)..(536)
180 <223> OTHER INFORMATION: amino acid sequence of non-receptor tyrosine kinase encoded
181 by the normal c-Src coding region
183 <400> SEQUENCE: 2
185 Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
186 1      5      10      15
189 Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
190      20      25      30
193 Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
194      35      40      45
197 Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
198      50      55      60

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201 Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
202 65 70 75 80
205 Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
206 85 90 95
209 Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
210 100 105 110
213 Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
214 115 120 125
217 Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
218 130 135 140
221 Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
222 145 150 155 160
225 Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
226 165 170 175
229 Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
230 180 185 190
233 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
234 195 200 205
237 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
238 210 215 220
241 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
242 225 230 235 240
245 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
246 245 250 255
249 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
250 260 265 270
253 Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr
254 275 280 285
257 Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr
258 290 295 300
261 Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu
262 305 310 315 320
265 Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
266 325 330 335
269 Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe
270 340 345 350
273 Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp
274 355 360 365
277 Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn
278 370 375 380
281 Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
282 385 390 395 400
285 Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
286 405 410 415
289 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
290 420 425 430
293 Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
294 435 440 445
297 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val

```

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```

298      450      455      460
301 Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg
302 465      470      475      480
305 Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
306      485      490      495
309 Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
310      500      505      510
313 Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
314      515      520      525
317 Gln Tyr Gln Pro Gly Glu Asn Leu
318      530      535
321 <210> SEQ ID NO: 3
322 <211> LENGTH: 1611
323 <212> TYPE: DNA
324 <213> ORGANISM: Homo sapiens
326 <220> FEATURE:
327 <221> NAME/KEY: misc_feature
328 <222> LOCATION: (1)..(1593)
329 <223> OTHER INFORMATION: nucleotide sequence of mutant c-Src oncogene coding region
332 <220> FEATURE:
333 <221> NAME/KEY: CDS
334 <222> LOCATION: (1)..(1593)
335 <223> OTHER INFORMATION:
338 <220> FEATURE:
339 <221> NAME/KEY: misc_feature
340 <222> LOCATION: (1591)..(1591)
341 <223> OTHER INFORMATION: Point mutation in normal c-Src causes transition from c-->t
and
342 the formation of a stop codon.
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346 atg ggt agc aac aag agc aag ccc aag gat gcc agc cag cgg cgc cgc      48
347 Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
348 1      5      10      15
350 agc ctg gag ccc gcc gag aac gtg cac ggc gct ggc ggg ggc gct ttc      96
351 Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
352      20      25      30
354 ccc gcc tcg cag acc ccc agc aag cca gcc tcg gcc gac ggc cac cgc      144
355 Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
356      35      40      45
358 ggc ccc agc gcg gcc ttc gcc ccc gcg gcc gcc gag ccc aag ctg ttc      192
359 Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
360      50      55      60
362 gga ggc ttc aac tcc tcg gac acc gtc acc tcc ccg cag agg gcg ggc      240
363 Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
364 65      70      75      80
366 ccg ctg gcc ggt gga gtg acc acc ttt gtg gcc ctc tat gac tat gag      288
367 Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
368      85      90      95
370 tct agg acg gag aca gac ctg tcc ttc aag aaa ggc gag cgg ctc cag      336
371 Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/444,711A

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 15

**VERIFICATION SUMMARY**

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:34 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:31  
L:345 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:335  
L:648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0